WEST Search History

DATE: Wednesday, May 15, 2002

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,JPAB,EPAB,DWPI; PLUR=YES; OP=OR			
L5	l4 near10 triplex	3	L5
L4	l1 near5 (single adj strand$3)	76	L4
L3	L2 near10 (single adj strand$2)	1	L3
L2	L1 near10 (clon$4 or ligat$4)	118	L2
L1	(Rec adj A) or RecA	1406	L1

END OF SEARCH HISTORY

Turin et al
5707811

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Search Results - Record(s) 1 through 3 of 3 returned.

☐ 1. Document ID: US 6248530 B1

L5: Entry 1 of 3 File: USPT Jun 19, 2001

US-PAT-NO: 6248530
DOCUMENT-IDENTIFIER: US 6248530 B1

TITLE: Method for eliminating specific sequences when constructing DNA libraries

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

☐ 2. Document ID: US 6114121 A

L5: Entry 2 of 3 File: USPT Sep 5, 2000

US-PAT-NO: 6114121
DOCUMENT-IDENTIFIER: US 6114121 A

does not teach.

TITLE: Nucleic acid probe molecule of hairpin-shape structure and method for detecting nucleic acids using the same

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

☐ 3. Document ID: US 5776744 A

L5: Entry 3 of 3 File: USPT Jul 7, 1998

US-PAT-NO: 5776744
DOCUMENT-IDENTIFIER: US 5776744 A

TITLE: Methods and compositions for effecting homologous recombination

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

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Terms	Documents
l4 near10 triplex	3

Display Format: - Change Format

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L4: Entry 1 of 76 File: USPT May 14, 2002

DOCUMENT-IDENTIFIER: US 6388169 B1
TITLE: Maize orthologues of bacterial RecA proteins

Brief Summary Paragraph Right (5):
It is well known that RecA binds single stranded DNA and promotes pairing and strand exchange between homologous DNA molecules. Reports of the use of bacterial RecA in association with DNA sequences to manipulate homologous target DNA, including improvement of the efficiency of gene targeting in non-plant systems, have been published (see, e.g., PCT published Patent Application Nos. WO 87/01730 and WO 93/22443).

End of Result Set

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L5: Entry 3 of 3 File: USPT Jul 7, 1998

DOCUMENT-IDENTIFIER: US 5776744 A
TITLE: Methods and compositions for effecting homologous recombination

Other Reference Publication (3):
Rao et al, "Homologous recognition and triplex formation promoted by RecA protein between duplex oligonucleotides and single-stranded DNA", J. Mol. Biol. 229:228-343, 1993.

This does not necessarily apply to the limitations claimed because the 3rd strand that forms the triplex w/ the ds DNA & RecA is an oligo not an ss overhanging end of a double-stranded DNA as claimed.

Moreover, I don't think they can get over 102 w/ A+B. These are their own publications >1yr b4 filing date.

X?

End of Result Set

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L5: Entry 3 of 3 File: USPT Jul 7, 1998

US-PAT-NO: 5776744
DOCUMENT-IDENTIFIER: US 5776744 A

TITLE: Methods and compositions for effecting homologous recombination

DATE-ISSUED: July 7, 1998

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Glazer; Peter M.	Guilford	CT		
Lin; L. Michael	Wilmington	DE		
George; Jay	Gaithersburg	MD		

US-CL-CURRENT: 435/463; 435/465, 435/5, 435/6, 435/91.1, 435/91.2

CLAIMS:

What is claimed is:

1. A method for effecting homologous recombination between a native nucleic acid segment in a cell and a donor nucleic acid segment introduced into the cell, which comprises:

a) introducing into a cell: i) an oligonucleotide third strand which comprises a base sequence capable of forming a triple helix at a binding region on one or both strands of a native nucleic acid segment in the vicinity of a target region where the recombination is to occur, said oligonucleotide being capable of inducing homologous recombination at the target region of the native nucleic acid, and ii) a donor nucleic acid which comprises a nucleic acid sequence sufficiently homologous to the native nucleic acid segment such that the donor sequence is capable of undergoing homologous recombination with the native sequence at the target region;

b) allowing the oligonucleotide to bind to the native nucleic acid segment to form a triple stranded nucleic acid, thereby inducing homologous recombination at the native nucleic acid segment target region; and

c) allowing homologous recombination to occur between the native and donor nucleic acid segments wherein the oligonucleotide third strand has a dissociation constant for the binding region of less than or equal to about 10.sup.-7 M.

2. The method of claim 1, wherein the oligonucleotide third strand is from about 7 to about 50 nucleotides in length.

3. The method of claim 2, wherein the oligonucleotide third strand is from about 10 to about 30 nucleotides in length.

4. The method of claim 1, wherein the oligonucleotide third strand contains an at least partially artificial backbone.

5. The method of claim 1, wherein the oligonucleotide third strand contains a backbone selected from the group consisting of phosphodiester, phosphorothioate, methyl phosphonate, peptide, and mixtures thereof.

6. The method of claim 5, wherein the backbone is phosphodiester.

7. The method of claim 1, wherein the oligonucleotide third strand is modified with one or more protective groups.

8. The method of claim 7, wherein the 3' and 5' ends of the oligonucleotide third strand are modified with one or more protective groups.

9. The method of claim 7, wherein the protective group is selected from the group consisting of alkyl amines, acridine and cholesterol.

10. The method of claim 1, wherein the oligonucleotide third strand is circularized.

11. The method of claim 1, wherein the oligonucleotide third strand contains at least one modified sugar.

12. The method of claim 1, wherein the oligonucleotide third strand comprises at least one synthetic base.

13. The method of claim 1, wherein the dissociation constant is less than or equal to about 2.times.10.sup.-8 M.

14. The method of claim 1, wherein the oligonucleotide third strand has linked thereto a moiety which induces the homologous recombination.

15. The method of claim 14, wherein the moiety is linked to the oligonucleotide directly.

16. The method of claim 14, wherein the moiety is linked to the oligonucleotide through a linker.

17. The method of claim 14, wherein the moiety is selected from the group consisting of acridine, psoralen, a substituted psoralen, hydroxymethylpsoralen, mitomycin C, 1-nitrosopyrene, a nuclease, a restriction enzyme, a radionuclide, boron, and iodine.

18. The method of claim 1, wherein the donor nucleic acid is double stranded.

19. The method of claim 1, wherein the donor nucleic acid is single stranded.

20. The method of claim 1, wherein the donor nucleic acid comprises two substantially complementary single strands.

21. The method of claim 1, wherein the donor nucleic acid is substantially homologous with the native nucleic acid.

22. The method of claim 21, wherein the donor nucleic acid is substantially homologous with the native nucleic acid in a region of about 20 bases at each end of the donor nucleic acid.

23. The method of claim 1, wherein the donor nucleic acid is at least about 40 bases in length.

24. The method of claim 23, wherein the donor nucleic acid is between about 40 and about 40,000 bases in length.

25. The method of claim 1, wherein the donor nucleic acid is introduced into the cell in the form of a packaging system.

26. The method of claim 25, wherein the packaging system is selected from the group consisting of a DNA virus, an RNA virus, and a liposome.

27. The method of claim 1, wherein the native nucleic acid contains a mutation that is corrected by the homologous recombination.

28. The method of claim 27, wherein the mutation is selected from the group consisting of base changes, deletions, insertions, nucleotide repeats, and combinations thereof.

29. The method of claim 1, wherein the homologous recombination causes an alteration in the native nucleic acid sequence.

30. The method of claim 29, wherein the alteration is an addition of a segment selected from the group consisting of a gene, a part of a gene, a gene control region, an intron, a splice junction, a transposable element, a site specific recombination sequence, and combinations thereof.

31. The method of claim 1, wherein the native nucleic acid is chromosomal.

32. The method of claim 1, wherein the native nucleic acid is extrachromosomal.

33. The method of claim 32, wherein the native nucleic acid is selected from the group consisting of mitochondrial, episomal, a plasmid and a chloroplast.

34. A method for effecting homologous recombination between a first nucleic acid segment in a cell and a donor nucleic acid segment introduced into the cell, which comprises:

a) contacting a donor nucleic acid segment with an oligonucleotide third strand which comprises a base sequence capable of forming a triple helix at a binding region on one or both strands of the donor nucleic acid segment in the vicinity of a target region where the recombination is to occur, said oligonucleotide being capable of inducing homologous recombination at the target region of the donor nucleic acid, and said donor having a sequence sufficiently homologous to a first nucleic acid segment such that the donor sequence will undergo homologous recombination with the first sequence at the target region;

b) allowing the oligonucleotide to bind to the donor nucleic acid segment to form a triple stranded nucleic acid, thereby treating the donor nucleic acid segment to make it capable of inducing homologous recombination at the donor nucleic acid segment target region;

c) introducing into a cell the treated donor nucleic acid; and

d) allowing homologous recombination to occur between the first and donor nucleic acid segments wherein the oligonucleotide third strand has a dissociation constant for the binding region of less than or equal to about 10.sup.-7 M.

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L5: Entry 1 of 3 File: USPT Jun 19, 2001

US-PAT-NO: 6248530
DOCUMENT-IDENTIFIER: US 6248530 B1

TITLE: Method for eliminating specific sequences when constructing DNA libraries

DATE-ISSUED: June 19, 2001

US-CL-CURRENT: 435/6; 536/23.1, 536/24.3

APPL-NO: 9/ 331709 [PALM]
DATE FILED: July 23, 1999

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	APPL-DATE
FR	96 15854	December 23, 1996

PCT-DATA:

APPL-NO	DATE-FILED	PUB-NO	PUB-DATE	371-DATE	102(E)-DATE
PCT/FR97/02378	December 22, 1997	WO98/28439	Jul 2, 1998	Jul 23, 1999	Jul 23, 1999

Generate Collection

L5: Entry 1 of 3 File: USPT Jun 19, 2001

US-PAT-NO: 6248530
DOCUMENT-IDENTIFIER: US 6248530 B1

TITLE: Method for eliminating specific sequences when constructing DNA libraries

DATE-ISSUED: June 19, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Nahas; Nasri	Paris			FRX
Dumas Milne Edwards; Jean-Baptiste	Paris			FRX

US-CL-CURRENT: 435/6; 536/23.1, 536/24.3

CLAIMS:

What is claimed is:

1. A method for selecting nucleic acids lacking at least one target sequence from a population of double stranded nucleic acids wherein said population includes double stranded nucleic acids comprising said target sequence and double stranded nucleic acids lacking said target sequence, said method comprising:

contacting said population of double stranded nucleic acids with at least one nucleic acid which hybridizes to said at least one target sequence under conditions in which said at least one nucleic acid which hybridizes to said at least one target sequence forms a triplex with said double stranded nucleic acids containing said at least one target sequence, wherein said at least one nucleic acid which hybridizes to said at least one target sequence has at least one restriction site recognized by a methylation sensitive restriction enzyme;

performing a methylation reaction on said population of double stranded nucleic acids;

dissociating said at least one nucleic acid which hybridizes to said at least one target sequence from said at least one target sequence;

performing a restriction digest with at least one methylation sensitive enzyme which cleaves at said at least one restriction site, wherein said double stranded nucleic acids containing said target sequence are cleaved by said at least one restriction enzyme while double stranded nucleic acids lacking said at least one target sequence are not cleaved by said at least one restriction enzyme; and

selectively recovering double stranded nucleic acids which were not cleaved by said at least one restriction enzyme.

2. The method of claim 1 wherein said selectively recovering step comprises introducing said population of double stranded nucleic acids into a suitable host cell wherein double stranded nucleic acids which were cleaved by said restriction enzyme do not replicate in said host cell and double stranded nucleic acids which were not cleaved by said restriction enzyme replicate in said host cell.

3. The method of claim 1, wherein said double stranded nucleic acids are plasmids.

4. The method of claim 1, wherein said at least one nucleic acid which hybridizes to said at least one target sequence is a peptide nucleic acid.

5. The method of claim 1, wherein said population of double stranded nucleic acids is a DNA library.

6. The method of claim 1, wherein said population of double stranded nucleic acids is a cDNA library.

7. The method of claim 1, wherein nucleic acids lacking one target sequence are selectively recovered.

8. The method of claim 1, wherein nucleic acids lacking several target sequences are selectively recovered.

9. The method of claim 1, wherein nucleic acids lacking a target sequence that is abundant are selectively recovered.

10. The method of claim 1, wherein nucleic acids lacking several target sequences that are abundant are selectively recovered.

11. The method of claim 1, wherein the triplex is formed in the presence of divalent cations.

12. The method of claim 1, wherein the triplex is formed in the presence of ATP.gamma.S.

13. The method of claim 1, wherein the methylation step is carried out by methyltransferases.

14. The method of claim 1, wherein the methylation sensitive restriction enzyme is selected from the group consisting of HaeIII and MspI.

15. The method of claim 1, wherein the nucleic acids which were cleaved by said restriction enzyme are eliminated by hydrolysis.

16. The method of claim 15, wherein the hydrolysis is carried out by an exonuclease.

17. A method for selecting nucleic acids lacking at least one target sequence from a population of double stranded nucleic acids wherein said population includes double stranded nucleic acids comprising said at least one target sequence and double stranded nucleic acids lacking said at least one target sequence, said method comprising:

contacting said population of double stranded nucleic acids with at least one single stranded nucleic acid which hybridizes to said at least one target sequence, wherein said at least one single stranded nucleic acid which hybridizes to said at least one target sequence has at least one restriction site recognized by a methylation sensitive restriction enzyme and is complexed with a protein which facilitates formation of a triplex comprising said at least one single stranded nucleic acid and said at least one target sequence;

performing a methylation reaction on said population of double stranded nucleic acids;

dissociating said at least one single stranded nucleic acid which hybridizes to said at least one target sequence from said at least one target sequence;

performing a restriction digest with at least one methylation sensitive enzyme which cleaves at said at least one restriction site, wherein said double stranded nucleic acids containing said at least one target sequence are cleaved by said restriction enzyme while double stranded nucleic acids lacking said at least one target sequence are not cleaved by said at least one restriction enzyme; and

selectively recovering double stranded nucleic acids which were not cleaved by said at least one restriction enzyme.

18. The method of claim 17 wherein said selectively recovering step comprises introducing said population of double stranded nucleic acids into a suitable host cell

wherein double stranded nucleic acids which were cleaved by said at least one restriction enzyme do not replicate in said host cell and double stranded nucleic acids which were not cleaved by said at least one restriction enzyme replicate in said host cell.

19. The method of claim 17 wherein said double stranded nucleic acids are plasmids.

20. The method of claim 17, wherein said at least one nucleic acid which hybridizes to said at least one target sequence is a peptide nucleic acid.

21. The method of claim 17, wherein said population of double stranded nucleic acids is a DNA library.

22. The method of claim 17, wherein said population of double stranded nucleic acids is a cDNA library.

23. The method of claim 17, wherein nucleic acids lacking one target sequence are selectively recovered.

24. The method of claim 17, wherein nucleic acids lacking several target sequences are selectively recovered.

25. The method of claim 17, wherein nucleic acids lacking a target sequence that is abundant are selectively recovered.

26. The method of claim 17, wherein nucleic acids having several target sequences that are abundant are separated from nucleic acids lacking said target sequences.

27. The method of claim 17, wherein the triplex is formed in the presence of divalent cations.

28. The method of claim 17, wherein the triplex is formed in the presence of ATP.gamma.S.

29. The method of claim 17, wherein the methylation step is carried out by methyltransferases.

30. The method of claim 17, wherein the methylation sensitive restriction enzyme is selected from the group consisting of HaeIII and MspI.

31. The method of claim 17, wherein the nucleic acids which were cleaved by said at least one restriction enzyme are eliminated by hydrolysis.

32. The method of claim 31, wherein the hydrolysis is carried out by an exonuclease.

33. The method of claim 17, wherein the protein which facilitates formation of a triplex comprising said at least one single stranded nucleic acid and said at least one target sequence is RecA.

Generate Collection

L5: Entry 1 of 3 File: USPT Jun 19, 2001

DOCUMENT-IDENTIFIER: US 6248530 B1
TITLE: Method for eliminating specific sequences when constructing DNA libraries

Brief Summary Paragraph Right (18):
In this method, the binding of a protein, in particular the RecA protein, to an appropriate single-strand DNA molecule catalyzes the formation of a triplex between this single-strand DNA (oligonucleotide) and a corresponding double-strand DNA; the triplex thus formed protects the sequences involved therein from methylation.

Generate Collection

L5: Entry 2 of 3 File: USPT Sep 5, 2000

US-PAT-NO: 6114121
DOCUMENT-IDENTIFIER: US 6114121 A

TITLE: Nucleic acid probe molecule of hairpin-shape structure and method for detecting nucleic acids using the same

DATE-ISSUED: September 5, 2000

US-CL-CURRENT: 435/6; 536/23.1, 536/24.3

APPL-NO: 8/ 969320 [PALM]
DATE FILED: November 13, 1997

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	APPL-DATE
JP	8-316906	November 14, 1996